



SEQUENCE LISTING

<110> Fujisawa Pharmaceutical Co., Ltd.
Matsuoka, Hideaki
Fujimura, Takao
Hayashi, Masako
Aramori, Ichiro

<120> New methods for selecting an immunosuppressive agent

<130> 274130US0PCT

<140> 10/540,546

<141> 2005-06-24

<150> JP2002-378800

<151> 2002-12-27

<160> 86

<170> PatentIn version 3.1

<210> 1

<211> 3255

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (1)..(3255)

<223> human histone deacetylase-4 (HDAC4) gene

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gtg	gag	ctg	ctg	aat	cct	gcc	cgc	gtg	aac	cac	atg	ccc	agc	acg	gtg	96
Val	Glu	Leu	Leu	Asn	Pro	Ala	Arg	Val	Asn	His	Met	Pro	Ser	Thr	Val	
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gat	gtg	gcc	acg	gcg	ctg	cct	ctg	caa	gtg	gcc	ccc	tcg	gca	gtg	ccc	144
Asp	Val	Ala	Thr	Ala	Leu	Pro	Leu	Gln	Val	Ala	Pro	Ser	Ala	Val	Pro	
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atg	gac	ctg	cgc	ctg	gac	cac	cag	ttc	tca	ctg	cct	gtg	gca	gag	ccg	192
Met	Asp	Leu	Arg	Leu	Asp	His	Gln	Phe	Ser	Leu	Pro	Val	Ala	Glu	Pro	
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gcc	ctg	cgg	gag	cag	cag	ctg	cag	cag	gag	ctc	ctg	gcg	ctc	aag	cag	240
Ala	Leu	Arg	Glu	Gln	Gln	Leu	Gln	Gln	Glu	Leu	Leu	Ala	Leu	Lys	Gln	
65				70					75					80		

aag	cag	cag	atc	cag	agg	cag	atc	ctc	atc	gct	gag	ttc	cag	agg	cag	288
Lys	Gln	Gln	Ile	Gln	Arg	Gln	Ile	Leu	Ile	Ala	Glu	Phe	Gln	Arg	Gln	
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cac	gag	cag	ctc	tcc	cgg	cag	cac	gag	gcg	cag	ctc	cac	gag	cac	atc	336
His	Glu	Gln	Leu	Ser	Arg	Gln	His	Glu	Ala	Gln	Leu	His	Glu	His	Ile	
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aag	caa	caa	cag	gag	atg	ctg	gcc	atg	aag	cac	cag	cag	gag	ctg	ctg	384
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Lys	Gln	Gln	Gln	Glu	Met	Leu	Ala	Met	Lys	His	Gln	Gln	Glu	Leu	Leu		
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Glu	His	Gln	Arg	Lys	Leu	Glu	Arg	His	Arg	Gln	Glu	Gln	Glu	Leu	Glu		
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Lys	Gln	His	Arg	Glu	Gln	Lys	Leu	Gln	Gln	Leu	Lys	Asn	Lys	Glu	Lys		
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Gly	Lys	Glu	Ser	Ala	Val	Ala	Ser	Thr	Glu	Val	Lys	Met	Lys	Leu	Gln		
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gaa	ttt	gtc	ctc	aat	aaa	aag	aag	gcg	ctg	gcc	cac	cgg	aat	ctg	aac	576	
Glu	Phe	Val	Leu	Asn	Lys	Lys	Lys	Ala	Leu	Ala	His	Arg	Asn	Leu	Asn		
			180					185					190				
cac	tgc	att	tcc	agc	gac	cct	cgc	tac	tgg	tac	ggg	aaa	acg	cag	cac	624	
His	Cys	Ile	Ser	Ser	Asp	Pro	Arg	Tyr	Trp	Tyr	Gly	Lys	Thr	Gln	His		
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agt	tcc	ctt	gac	cag	agt	tct	cca	ccc	cag	agc	gga	gtg	tcg	acc	tcc	672	
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Tyr	Asn	His	Pro	Val	Leu	Gly	Met	Tyr	Asp	Ala	Lys	Asp	Asp	Phe	Pro		
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ctt	agg	aaa	aca	gct	tct	gaa	ccg	aat	ctg	aaa	tta	cgg	tcc	agg	cta	768	
Leu	Arg	Lys	Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Leu	Arg	Ser	Arg	Leu		
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Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys		
			260				265						270				
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Asp	Gly	Pro	Val	Val	Thr	Ala	Leu	Lys	Lys	Arg	Pro	Leu	Asp	Val	Thr		
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gac	tcc	gcg	tgc	agc	agc	gcc	cca	ggc	tcc	gga	ccc	agc	tca	ccc	aac	912	
Asp	Ser	Ala	Cys	Ser	Ser	Ala	Pro	Gly	Ser	Gly	Pro	Ser	Ser	Pro	Asn		
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Pro	Ser	Ile	Pro	Ala	Glu	Thr	Ser	Leu	Ala	His	Arg	Leu	Val	Ala	Arg		
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Glu	Gly	Ser	Ala	Ala	Pro	Leu	Pro	Leu	Tyr	Thr	Ser	Pro	Ser	Leu	Pro		
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ccc ttg gag cgg gac gga ggg gca gcg cac agc cct ctt ctg cag cac Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His			1248
405	410	415	
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435	440	445	
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465	470	475	480
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485	490	495	
ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc Phe Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser			1536
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gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu			1584
515	520	525	
ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu			1632
530	535	540	
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580	585	590	
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aaa ctt cta ggc tcg ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly 740 745 750	2256
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gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 980 985 990	2976
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg 995 1000 1005	3024
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tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val 1045 1050 1055	3168
acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg 1060 1065 1070	3216
cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu 1075 1080	3255

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 35 40 45
 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60
 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 65 70 75 80
 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 85 90 95
 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110
 Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
 115 120 125
 Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
 130 135 140
 Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
 145 150 155 160
 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175
 Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190
 His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205
 Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220
 Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
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 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn

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Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg 325 330 335		
Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro 340 345 350		
Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala 355 360 365		
Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg 370 375 380		
Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser 385 390 395 400		
Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His 405 410 415		
Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly 420 425 430		
Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg 435 440 445		
Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg 450 455 460		
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Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln 485 490 495		
Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser 500 505 510		
Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu 515 520 525		
Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu 530 535 540		
Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln 545 550 555 560		
Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val 565 570 575		
Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln 580 585 590		
Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr 595 600 605		
Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His 610 615 620		

Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro
 625 630 635 640
 Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu
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 Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser
 660 665 670
 Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
 675 680 685
 Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg
 690 695 700
 Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr
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 Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys
 770 775 780
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 Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
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 820 825 830
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 835 840 845
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 850 855 860
 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
 865 870 875 880
 Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
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 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
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 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
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Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
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 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
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 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005
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 <212> DNA
 <213> Artificial Sequence

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 <223> Dominant negative mutant (H802K, H803L) of human histone deacetylase-4
 (HDAC4) gene

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 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
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 atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg 192
 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60

 gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag 240
 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 65 70 75 80

 aag cag cag atc cag agg cag atc ctc atc gct gag ttc cag agg cag 288

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His	Glu	Gln	Leu	Ser	Arg	Gln	His	Glu	Ala	Gln	Leu	His	Glu	His	Ile		
			100					105					110				
aag	caa	caa	cag	gag	atg	ctg	gcc	atg	aag	cac	cag	cag	gag	ctg	ctg		384
Lys	Gln	Gln	Gln	Glu	Met	Leu	Ala	Met	Lys	His	Gln	Gln	Glu	Leu	Leu		
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aag	cag	cac	cgg	gag	cag	aag	ctg	cag	cag	ctc	aag	aac	aag	gag	aag		480
Lys	Gln	His	Arg	Glu	Gln	Lys	Leu	Gln	Gln	Leu	Lys	Asn	Lys	Glu	Lys		
	145				150					155					160		
ggc	aaa	gag	agt	gcc	gtg	gcc	agc	aca	gaa	gtg	aag	atg	aag	tta	caa		528
Gly	Lys	Glu	Ser	Ala	Val	Ala	Ser	Thr	Glu	Val	Lys	Met	Lys	Leu	Gln		
			165					170						175			
gaa	ttt	gtc	ctc	aat	aaa	aag	aag	gcg	ctg	gcc	cac	cgg	aat	ctg	aac		576
Glu	Phe	Val	Leu	Asn	Lys	Lys	Lys	Ala	Leu	Ala	His	Arg	Asn	Leu	Asn		
			180					185					190				
cac	tgc	att	tcc	agc	gac	cct	cgc	tac	tgg	tac	ggg	aaa	acg	cag	cac		624
His	Cys	Ile	Ser	Ser	Asp	Pro	Arg	Tyr	Trp	Tyr	Gly	Lys	Thr	Gln	His		
		195				200						205					
agt	tcc	ctt	gac	cag	agt	tct	cca	ccc	cag	agc	gga	gtg	tcg	acc	tcc		672
Ser	Ser	Leu	Asp	Gln	Ser	Ser	Pro	Pro	Gln	Ser	Gly	Val	Ser	Thr	Ser		
	210					215					220						
tat	aac	cac	ccg	gtc	ctg	gga	atg	tac	gac	gcc	aaa	gat	gac	ttc	cct		720
Tyr	Asn	His	Pro	Val	Leu	Gly	Met	Tyr	Asp	Ala	Lys	Asp	Asp	Phe	Pro		
	225				230				235						240		
ctt	agg	aaa	aca	gct	tct	gaa	ccg	aat	ctg	aaa	tta	cgg	tcc	agg	cta		768
Leu	Arg	Lys	Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Leu	Arg	Ser	Arg	Leu		
			245					250						255			
aag	cag	aaa	gtg	gcc	gaa	aga	cgg	agc	agc	ccc	ctg	tta	cgc	agg	aaa		816
Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys		
			260				265						270				
gac	ggg	cca	gtg	gtc	act	gct	cta	aaa	aag	cgt	ccg	ttg	gat	gtc	aca		864
Asp	Gly	Pro	Val	Val	Thr	Ala	Leu	Lys	Lys	Arg	Pro	Leu	Asp	Val	Thr		
		275					280					285					
gac	tcc	gcg	tgc	agc	agc	gcc	cca	ggc	tcc	gga	ccc	agc	tca	ccc	aac		912
Asp	Ser	Ala	Cys	Ser	Ser	Ala	Pro	Gly	Ser	Gly	Pro	Ser	Ser	Pro	Asn		
	290					295					300						
aac	agc	tcc	ggg	agc	gtc	agc	gcg	gag	aac	ggt	atc	gcg	ccc	gcc	gtc		960
Asn	Ser	Ser	Gly	Ser	Val	Ser	Ala	Glu	Asn	Gly	Ile	Ala	Pro	Ala	Val		
	305				310				315						320		
ccc	agc	atc	ccg	gcg	gag	acg	agt	ttg	gcg	cac	aga	ctt	gtg	gca	cga		1008
Pro	Ser	Ile	Pro	Ala	Glu	Thr	Ser	Leu	Ala	His	Arg	Leu	Val	Ala	Arg		

325										330					335					
gaa ggc tcg gcc gct cca ctt ccc ctc tac aca tcg cca tcc ttg ccc	1056																			
Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro																				
340 345 350																				
aac atc acg ctg ggc ctg cct gcc acc ggc ccc tct gcg ggc acg gcg	1104																			
Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala																				
355 360 365																				
ggc cag cag gac acc gag aga ctc acc ctt ccc gcc ctc cag cag agg	1152																			
Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg																				
370 375 380																				
ctc tcc ctt ttc ccc ggc acc cac ctc act ccc tac ctg agc acc tcg	1200																			
Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser																				
385 390 395 400																				
ccc ttg gag cgg gac gga ggg gca gcg cac agc cct ctt ctg cag cac	1248																			
Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His																				
405 410 415																				
atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctc gtc aca ggc	1296																			
Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly																				
420 425 430																				
ctg gga gca ctg ccc ctc cac gca cag tcc ttg gtt ggt gca gac cgg	1344																			
Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg																				
435 440 445																				
gtg tcc ccc tcc atc cac aag ctg cgg cag cac cgc cca ctg ggg cgg	1392																			
Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg																				
450 455 460																				
acc cag tcg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg	1440																			
Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu																				
465 470 475 480																				
gtc atc cag cag cag cat cag cag ttt ctg gag aaa cac aag cag cag	1488																			
Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln																				
485 490 495																				
ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc	1536																			
Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser																				
500 505 510																				
gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag	1584																			
Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu																				
515 520 525																				
ctc cgt gag cac cag gct ctg ctg gac gag ccc tac ctg gac cgg ctg	1632																			
Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu																				
530 535 540																				
ccg ggg cag aag gag gcg cac gca cag gcc ggc gtg cag gtg aag cag	1680																			
Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln																				
545 550 555 560																				
gag ccc att gag agc gat gag gaa gag gca gag ccc cca cgg gag gtg	1728																			
Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val																				
565 570 575																				

gag ccg ggc cag cgc cag ccc agt gag cag gag ctg ctc ttc aga cag	1776
Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln	
580 585 590	
caa gcc ctc ctg ctg gag cag cag cgg atc cac cag ctg agg aac tac	1824
Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr	
595 600 605	
cag gcg tcc atg gag gcc gcc ggc atc ccc gtg tcc ttc ggc ggc cac	1872
Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His	
610 615 620	
agg cct ctg tcc cgg gcg cag tcc tca ccc gcg tct gcc acc ttc ccc	1920
Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro	
625 630 635 640	
gtg tct gtg cag gag ccc ccc acc aag ccg agg ttc acg aca ggc ctc	1968
Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu	
645 650 655	
gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc	2016
Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser	
660 665 670	
agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc	2064
Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg	
675 680 685	
ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc	2112
Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg	
690 695 700	
aag gcc acc ctg gag gag cta cag acg gtg cac tcg gaa gcc cac acc	2160
Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr	
705 710 715 720	
ctc ctg tat ggc acg aac ccc ctc aac cgg cag aaa ctg gac agt aag	2208
Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys	
725 730 735	
aaa ctt cta ggc tcg ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt	2256
Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly	
740 745 750	
ggt gtt ggg gtg gac agt gac acc ata tgg aac gag gtg cac tcg gcg	2304
Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala	
755 760 765	
ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag	2352
Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys	
770 775 780	
gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct	2400
Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro	
785 790 795 800	
gga aag ctt gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac	2448
Gly Lys Leu Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn	
805 810 815	

tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser 820 825 830	2496
aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln 835 840 845	2544
cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc cac cgc Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg 850 855 860	2592
tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val 865 870 875 880	2640
ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly 885 890 895	2688
ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg 900 905 910	2736
acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu 915 920 925	2784
gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly 930 935 940	2832
ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu 945 950 955 960	2880
atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His 965 970 975	2928
gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu 980 985 990	2976
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg 995 1000 1005	3024
ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His 1010 1015 1020	3072
agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg tct ctg Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg 1025 1030 1035 1040	3120
tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val 1045 1050 1055	3168
acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga	3216

Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
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cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag 3255
 Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
 1075 1080

<210> 4
 <211> 1084
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dominant negative mutant (H802K, H803L) of human histone deacetylase-4
 (HDAC4) gene

<400> 4

Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
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Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30

Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
 35 40 45

Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
 50 55 60

Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
 65 70 75 80

Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
 85 90 95

His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
 100 105 110

Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
 115 120 125

Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
 130 135 140

Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
 145 150 155 160

Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175

Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190

His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205

Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220

Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
 260 265 270
 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
 290 295 300
 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
 305 310 315 320
 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
 325 330 335
 Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
 340 345 350
 Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
 355 360 365
 Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg
 370 375 380
 Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser
 385 390 395 400
 Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His
 405 410 415
 Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
 420 425 430
 Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg
 435 440 445
 Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg
 450 455 460
 Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu
 465 470 475 480
 Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln
 485 490 495
 Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser
 500 505 510
 Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu
 515 520 525
 Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu
 530 535 540
 Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln

545		550		555		560
Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val						
	565			570		575
Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln						
	580			585		590
Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr						
	595			600		605
Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His						
	610			615		620
Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro						
	625			630		640
Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu						
	645			650		655
Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser						
	660			665		670
Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg						
	675			680		685
Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg						
	690			695		700
Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr						
	705			710		715
Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys						
	725			730		735
Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly						
	740			745		750
Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala						
	755			760		765
Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys						
	770			775		780
Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro						
	785			790		795
Gly Lys Leu Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn						
	805			810		815
Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser						
	820			825		830
Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln						
	835			840		845
Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg						
	850			855		860
Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val						
	865			870		875
						880

Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
 885 890 895
 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
 900 905 910
 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
 915 920 925
 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
 930 935 940
 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
 945 950 955 960
 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
 965 970 975
 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
 980 985 990
 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005
 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
 1010 1015 1020
 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
 1025 1030 1035 1040
 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
 1045 1050 1055
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 1060 1065 1070
 Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
 1075 1080 1084

<210> 5
 <211> 3255
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> CDS
 <222> (1)..(3255)
 <223> Dominant negative mutant (H863L) of human histone deacetylase-4
 (HDAC4)
 gene

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 gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc agc acg gtg 96
 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
 20 25 30

gat	gtg	gcc	acg	gcg	ctg	cct	ctg	caa	gtg	gcc	ccc	tcg	gca	gtg	ccc	144
Asp	Val	Ala	Thr	Ala	Leu	Pro	Leu	Gln	Val	Ala	Pro	Ser	Ala	Val	Pro	
		35					40					45				
atg	gac	ctg	cgc	ctg	gac	cac	cag	ttc	tca	ctg	cct	gtg	gca	gag	ccg	192
Met	Asp	Leu	Arg	Leu	Asp	His	Gln	Phe	Ser	Leu	Pro	Val	Ala	Glu	Pro	
	50					55					60					
gcc	ctg	cgg	gag	cag	cag	ctg	cag	cag	gag	ctc	ctg	gcg	ctc	aag	cag	240
Ala	Leu	Arg	Glu	Gln	Gln	Leu	Gln	Gln	Glu	Leu	Leu	Ala	Leu	Lys	Gln	
65					70					75					80	
aag	cag	cag	atc	cag	agg	cag	atc	ctc	atc	gct	gag	ttc	cag	agg	cag	288
Lys	Gln	Gln	Ile	Gln	Arg	Gln	Ile	Leu	Ile	Ala	Glu	Phe	Gln	Arg	Gln	
				85				90						95		
cac	gag	cag	ctc	tcc	cgg	cag	cac	gag	gcg	cag	ctc	cac	gag	cac	atc	336
His	Glu	Gln	Leu	Ser	Arg	Gln	His	Glu	Ala	Gln	Leu	His	Glu	His	Ile	
			100					105					110			
aag	caa	caa	cag	gag	atg	ctg	gcc	atg	aag	cac	cag	cag	gag	ctg	ctg	384
Lys	Gln	Gln	Gln	Glu	Met	Leu	Ala	Met	Lys	His	Gln	Gln	Glu	Leu	Leu	
		115					120					125				
gaa	cac	cag	cgg	aag	ctg	gag	agg	cac	cgc	cag	gag	cag	gag	ctg	gag	432
Glu	His	Gln	Arg	Lys	Leu	Glu	Arg	His	Arg	Gln	Glu	Gln	Glu	Leu	Glu	
	130					135					140					
aag	cag	cac	cgg	gag	cag	aag	ctg	cag	cag	ctc	aag	aac	aag	gag	aag	480
Lys	Gln	His	Arg	Glu	Gln	Lys	Leu	Gln	Gln	Leu	Lys	Asn	Lys	Glu	Lys	
145					150					155					160	
ggc	aaa	gag	agt	gcc	gtg	gcc	agc	aca	gaa	gtg	aag	atg	aag	tta	caa	528
Gly	Lys	Glu	Ser	Ala	Val	Ala	Ser	Thr	Glu	Val	Lys	Met	Lys	Leu	Gln	
				165					170					175		
gaa	ttt	gtc	ctc	aat	aaa	aag	aag	gcg	ctg	gcc	cac	cgg	aat	ctg	aac	576
Glu	Phe	Val	Leu	Asn	Lys	Lys	Lys	Ala	Leu	Ala	His	Arg	Asn	Leu	Asn	
			180					185					190			
cac	tgc	att	tcc	agc	gac	cct	cgc	tac	tgg	tac	ggg	aaa	acg	cag	cac	624
His	Cys	Ile	Ser	Ser	Asp	Pro	Arg	Tyr	Trp	Tyr	Gly	Lys	Thr	Gln	His	
		195				200						205				
agt	tcc	ctt	gac	cag	agt	tct	cca	ccc	cag	agc	gga	gtg	tcg	acc	tcc	672
Ser	Ser	Leu	Asp	Gln	Ser	Ser	Pro	Pro	Gln	Ser	Gly	Val	Ser	Thr	Ser	
	210					215					220					
tat	aac	cac	ccg	gtc	ctg	gga	atg	tac	gac	gcc	aaa	gat	gac	ttc	cct	720
Tyr	Asn	His	Pro	Val	Leu	Gly	Met	Tyr	Asp	Ala	Lys	Asp	Asp	Phe	Pro	
225					230					235					240	
ctt	agg	aaa	aca	gct	tct	gaa	ccg	aat	ctg	aaa	tta	cgg	tcc	agg	cta	768
Leu	Arg	Lys	Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Leu	Arg	Ser	Arg	Leu	
				245					250					255		
aag	cag	aaa	gtg	gcc	gaa	aga	cgg	agc	agc	ccc	ctg	tta	cgc	agg	aaa	816
Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys	
			260					265					270			

gac ggg cca gtg gtc act gct cta aaa aag cgt ccg ttg gat gtc aca	864
Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr	
275 280 285	
gac tcc gcg tgc agc agc gcc cca ggc tcc gga ccc agc tca ccc aac	912
Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn	
290 295 300	
aac agc tcc ggg agc gtc agc gcg gag aac ggt atc gcg ccc gcc gtc	960
Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val	
305 310 315 320	
ccc agc atc ccg gcg gag acg agt ttg gcg cac aga ctt gtg gca cga	1008
Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg	
325 330 335	
gaa ggc tcg gcc gct cca ctt ccc ctc tac aca tcg cca tcc ttg ccc	1056
Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro	
340 345 350	
aac atc acg ctg ggc ctg cct gcc acc ggc ccc tct gcg ggc acg gcg	1104
Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala	
355 360 365	
ggc cag cag gac acc gag aga ctc acc ctt ccc gcc ctc cag cag agg	1152
Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg	
370 375 380	
ctc tcc ctt ttc ccc ggc acc cac ctc act ccc tac ctg agc acc tcg	1200
Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser	
385 390 395 400	
ccc ttg gag cgg gac gga ggg gca gcg cac agc cct ctt ctg cag cac	1248
Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His	
405 410 415	
atg gtc tta ctg gag cag cca ccg gca caa gca ccc ctc gtc aca ggc	1296
Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly	
420 425 430	
ctg gga gca ctg ccc ctc cac gca cag tcc ttg gtt ggt gca gac cgg	1344
Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg	
435 440 445	
gtg tcc ccc tcc atc cac aag ctg cgg cag cac cgc cca ctg ggg cgg	1392
Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg	
450 455 460	
acc cag tcg gcc ccg ctg ccc cag aac gcc cag gct ctg cag cac ctg	1440
Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu	
465 470 475 480	
gtc atc cag cag cag cat cag cag ttt ctg gag aaa cac aag cag cag	1488
Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln	
485 490 495	
ttc cag cag cag caa ctg cag atg aac aag atc atc ccc aag cca agc	1536
Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser	
500 505 510	
gag cca gcc cgg cag ccg gag agc cac ccg gag gag acg gag gag gag	1584

Glu	Pro	Ala	Arg	Gln	Pro	Glu	Ser	His	Pro	Glu	Glu	Thr	Glu	Glu	Glu		
		515					520					525					
ctc	cgt	gag	cac	cag	gct	ctg	ctg	gac	gag	ccc	tac	ctg	gac	cgg	ctg	1632	
Leu	Arg	Glu	His	Gln	Ala	Leu	Leu	Asp	Glu	Pro	Tyr	Leu	Asp	Arg	Leu		
		530					535				540						
ccg	ggg	cag	aag	gag	gcg	cac	gca	cag	gcc	ggc	gtg	cag	gtg	aag	cag	1680	
Pro	Gly	Gln	Lys	Glu	Ala	His	Ala	Gln	Ala	Gly	Val	Gln	Val	Lys	Gln		
		545				550				555					560		
gag	ccc	att	gag	agc	gat	gag	gaa	gag	gca	gag	ccc	cca	cgg	gag	gtg	1728	
Glu	Pro	Ile	Glu	Ser	Asp	Glu	Glu	Glu	Ala	Glu	Pro	Pro	Arg	Glu	Val		
				565					570					575			
gag	ccg	ggc	cag	cgc	cag	ccc	agt	gag	cag	gag	ctg	ctc	ttc	aga	cag	1776	
Glu	Pro	Gly	Gln	Arg	Gln	Pro	Ser	Glu	Gln	Glu	Leu	Leu	Phe	Arg	Gln		
			580					585					590				
caa	gcc	ctc	ctg	ctg	gag	cag	cag	cgg	atc	cac	cag	ctg	agg	aac	tac	1824	
Gln	Ala	Leu	Leu	Leu	Glu	Gln	Gln	Arg	Ile	His	Gln	Leu	Arg	Asn	Tyr		
		595					600					605					
cag	gcg	tcc	atg	gag	gcc	gcc	ggc	atc	ccc	gtg	tcc	ttc	ggc	ggc	cac	1872	
Gln	Ala	Ser	Met	Glu	Ala	Ala	Gly	Ile	Pro	Val	Ser	Phe	Gly	Gly	His		
		610				615					620						
agg	cct	ctg	tcc	cgg	gcg	cag	tcc	tca	ccc	gcg	tct	gcc	acc	ttc	ccc	1920	
Arg	Pro	Leu	Ser	Arg	Ala	Gln	Ser	Ser	Pro	Ala	Ser	Ala	Thr	Phe	Pro		
		625				630				635					640		
gtg	tct	gtg	cag	gag	ccc	ccc	acc	aag	ccg	agg	ttc	acg	aca	ggc	ctc	1968	
Val	Ser	Val	Gln	Glu	Pro	Pro	Thr	Lys	Pro	Arg	Phe	Thr	Thr	Gly	Leu		
				645					650					655			
gtg	tat	gac	acg	ctg	atg	ctg	aag	cac	cag	tgc	acc	tgc	ggg	agt	agc	2016	
Val	Tyr	Asp	Thr	Leu	Met	Leu	Lys	His	Gln	Cys	Thr	Cys	Gly	Ser	Ser		
			660					665					670				
agc	agc	cac	ccc	gag	cac	gcc	ggg	agg	atc	cag	agc	atc	tgg	tcc	cgc	2064	
Ser	Ser	His	Pro	Glu	His	Ala	Gly	Arg	Ile	Gln	Ser	Ile	Trp	Ser	Arg		
		675					680					685					
ctg	cag	gag	acg	ggc	ctc	cgg	ggc	aaa	tgc	gag	tgc	atc	cgc	gga	cgc	2112	
Leu	Gln	Glu	Thr	Gly	Leu	Arg	Gly	Lys	Cys	Glu	Cys	Ile	Arg	Gly	Arg		
		690				695					700						
aag	gcc	acc	ctg	gag	gag	cta	cag	acg	gtg	cac	tgc	gaa	gcc	cac	acc	2160	
Lys	Ala	Thr	Leu	Glu	Glu	Leu	Gln	Thr	Val	His	Ser	Glu	Ala	His	Thr		
		705				710				715					720		
ctc	ctg	tat	ggc	acg	aac	ccc	ctc	aac	cgg	cag	aaa	ctg	gac	agt	aag	2208	
Leu	Leu	Tyr	Gly	Thr	Asn	Pro	Leu	Asn	Arg	Gln	Lys	Leu	Asp	Ser	Lys		
				725					730					735			
aaa	ctt	cta	ggc	tgc	ctc	gcc	tcc	gtg	ttc	gtc	cgg	ctc	cct	tgc	ggc	2256	
Lys	Leu	Leu	Gly	Ser	Leu	Ala	Ser	Val	Phe	Val	Arg	Leu	Pro	Cys	Gly		
			740					745					750				
ggc	gtt	ggg	gtg	gac	agt	gac	acc	ata	tgg	aac	gag	gtg	cac	tgc	gcg	2304	
Gly	Val	Gly	Val	Asp	Ser	Asp	Thr	Ile	Trp	Asn	Glu	Val	His	Ser	Ala		

755	760	765	
ggg gca gcc cgc ctg gct gtg	ggc tgc gtg gta gag ctg gtc ttc aag		2352
Gly Ala Ala Arg Leu Ala Val	Gly Cys Val Val Glu Leu Val Phe Lys		
770	775	780	
gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct			2400
Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro			
785	790	795	800
gga cac cat gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac			2448
Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn			
	805	810	815
tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc			2496
Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser			
	820	825	830
aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag			2544
Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln			
	835	840	845
cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc ctt cgc			2592
Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu Leu Arg			
	850	855	860
tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg			2640
Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val			
	865	870	875
ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc			2688
Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly			
	885	890	895
ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga			2736
Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg			
	900	905	910
acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg			2784
Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu			
	915	920	925
gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccc acc cct ctt ggg			2832
Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly			
	930	935	940
ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg			2880
Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu			
	945	950	955
atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac			2928
Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His			
	965	970	975
gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg			2976
Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu			
	980	985	990
ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga			3024
Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg			
	995	1000	1005

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ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac      3072
Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
    1010                      1015                      1020

agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg ggg cgt      3120
Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
    1025                      1030                      1035                      1040

tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc      3168
Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
    1045                      1050                      1055

acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga      3216
Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
    1060                      1065                      1070

cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag      3255
Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
    1075                      1080

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<210> 6
<211> 1084
<212> PRT
<213> Homo sapiens

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<220>
<223> Dominant negative mutant (H863L) of human histone deacetylase-4
(HDAC4)
      gene

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<400> 6

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Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
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Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
20          25          30

Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
35          40          45

Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
50          55          60

Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
65          70          75          80

Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
85          90          95

His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
100         105         110

Lys Gln Gln Gln Glu Met Leu Ala Met Lys His Gln Gln Glu Leu Leu
115         120         125

Glu His Gln Arg Lys Leu Glu Arg His Arg Gln Glu Gln Glu Leu Glu
130         135         140

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Lys Gln His Arg Glu Gln Lys Leu Gln Gln Leu Lys Asn Lys Glu Lys
 145 150 155 160
 Gly Lys Glu Ser Ala Val Ala Ser Thr Glu Val Lys Met Lys Leu Gln
 165 170 175
 Glu Phe Val Leu Asn Lys Lys Lys Ala Leu Ala His Arg Asn Leu Asn
 180 185 190
 His Cys Ile Ser Ser Asp Pro Arg Tyr Trp Tyr Gly Lys Thr Gln His
 195 200 205
 Ser Ser Leu Asp Gln Ser Ser Pro Pro Gln Ser Gly Val Ser Thr Ser
 210 215 220
 Tyr Asn His Pro Val Leu Gly Met Tyr Asp Ala Lys Asp Asp Phe Pro
 225 230 235 240
 Leu Arg Lys Thr Ala Ser Glu Pro Asn Leu Lys Leu Arg Ser Arg Leu
 245 250 255
 Lys Gln Lys Val Ala Glu Arg Arg Ser Ser Pro Leu Leu Arg Arg Lys
 260 265 270
 Asp Gly Pro Val Val Thr Ala Leu Lys Lys Arg Pro Leu Asp Val Thr
 275 280 285
 Asp Ser Ala Cys Ser Ser Ala Pro Gly Ser Gly Pro Ser Ser Pro Asn
 290 295 300
 Asn Ser Ser Gly Ser Val Ser Ala Glu Asn Gly Ile Ala Pro Ala Val
 305 310 315 320
 Pro Ser Ile Pro Ala Glu Thr Ser Leu Ala His Arg Leu Val Ala Arg
 325 330 335
 Glu Gly Ser Ala Ala Pro Leu Pro Leu Tyr Thr Ser Pro Ser Leu Pro
 340 345 350
 Asn Ile Thr Leu Gly Leu Pro Ala Thr Gly Pro Ser Ala Gly Thr Ala
 355 360 365
 Gly Gln Gln Asp Thr Glu Arg Leu Thr Leu Pro Ala Leu Gln Gln Arg
 370 375 380
 Leu Ser Leu Phe Pro Gly Thr His Leu Thr Pro Tyr Leu Ser Thr Ser
 385 390 395 400
 Pro Leu Glu Arg Asp Gly Gly Ala Ala His Ser Pro Leu Leu Gln His
 405 410 415
 Met Val Leu Leu Glu Gln Pro Pro Ala Gln Ala Pro Leu Val Thr Gly
 420 425 430
 Leu Gly Ala Leu Pro Leu His Ala Gln Ser Leu Val Gly Ala Asp Arg
 435 440 445
 Val Ser Pro Ser Ile His Lys Leu Arg Gln His Arg Pro Leu Gly Arg
 450 455 460
 Thr Gln Ser Ala Pro Leu Pro Gln Asn Ala Gln Ala Leu Gln His Leu

465		470		475		480
Val Ile Gln Gln Gln His Gln Gln Phe Leu Glu Lys His Lys Gln Gln						
		485		490		495
Phe Gln Gln Gln Gln Leu Gln Met Asn Lys Ile Ile Pro Lys Pro Ser						
		500		505		510
Glu Pro Ala Arg Gln Pro Glu Ser His Pro Glu Glu Thr Glu Glu Glu						
		515		520		525
Leu Arg Glu His Gln Ala Leu Leu Asp Glu Pro Tyr Leu Asp Arg Leu						
		530		535		540
Pro Gly Gln Lys Glu Ala His Ala Gln Ala Gly Val Gln Val Lys Gln						
		545		550		555
Glu Pro Ile Glu Ser Asp Glu Glu Glu Ala Glu Pro Pro Arg Glu Val						
		565		570		575
Glu Pro Gly Gln Arg Gln Pro Ser Glu Gln Glu Leu Leu Phe Arg Gln						
		580		585		590
Gln Ala Leu Leu Leu Glu Gln Gln Arg Ile His Gln Leu Arg Asn Tyr						
		595		600		605
Gln Ala Ser Met Glu Ala Ala Gly Ile Pro Val Ser Phe Gly Gly His						
		610		615		620
Arg Pro Leu Ser Arg Ala Gln Ser Ser Pro Ala Ser Ala Thr Phe Pro						
		625		630		635
Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu						
		645		650		655
Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser						
		660		665		670
Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg						
		675		680		685
Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg						
		690		695		700
Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr						
		705		710		715
Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys						
		725		730		735
Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly						
		740		745		750
Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala						
		755		760		765
Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys						
		770		775		780
Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro						
		785		790		795
						800

Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
 805 810 815
 Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser
 820 825 830
 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
 835 840 845
 Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu Leu Arg
 850 855 860
 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
 865 870 875 880
 Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
 885 890 895
 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
 900 905 910
 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
 915 920 925
 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
 930 935 940
 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
 945 950 955 960
 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
 965 970 975
 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
 980 985 990
 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
 995 1000 1005
 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
 1010 1015 1020
 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
 1025 1030 1035 1040
 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
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 Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
 1075 1080 1084

<210> 7
 <211> 1743
 <212> DNA
 <213> Homo sapiens

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<220>
<221> CDS
<222> (43)..(1176)
<223> human histone deacetylase-8 (HDAC8) gene

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                                         Met Glu Glu Pro
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gag gaa ccg gcg gac agt ggg cag tcg ctg gtc ccg gtt tat atc tat      102
Glu Glu Pro Ala Asp Ser Gly Gln Ser Leu Val Pro Val Tyr Ile Tyr
5                               10                               15                               20

agt ccc gag tat gtc agt atg tgt gac tcc ctg gcc aag atc ccc aaa      150
Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala Lys Ile Pro Lys
25                               30                               35

cgg gcc agt atg gtg cat tct ttg att gaa gca tat gca ctg cat aag      198
Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr Ala Leu His Lys
40                               45                               50

cag atg agg ata gtt aag cct aaa gtg gcc tcc atg gag gag atg gcc      246
Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met Glu Glu Met Ala
55                               60                               65

acc ttc cac act gat gct tat ctg cag cat ctc cag aag gtc agc caa      294
Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln Lys Val Ser Gln
70                               75                               80

gag ggc gat gat gat cat ccg gac tcc ata gaa tat ggg cta ggt tat      342
Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr Gly Leu Gly Tyr
85                               90                               95                               100

gac tgc cca gcc act gaa ggg ata ttt gac tat gca gca gct ata gga      390
Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala Ala Ala Ile Gly
105                               110                               115

ggg gct acg atc aca gct gcc caa tgc ctg att gac gga atg tgc aaa      438
Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp Gly Met Cys Lys
120                               125                               130

gta gca att aac tgg tct gga ggg tgg cat cat gca aag aaa gat gaa      486
Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala Lys Lys Asp Glu
135                               140                               145

gca tct ggt ttt tgt tat ctc aat gat gct gtc ctg gga ata tta cga      534
Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu Gly Ile Leu Arg
150                               155                               160

ttg cga cgg aaa ttt gag cgt att ctc tac gtg gat ttg gat ctg cac      582
Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp Leu Asp Leu His
165                               170                               175                               180

cat gga gat ggt gta gaa gac gca ttc agt ttc acc tcc aaa gtc atg      630
His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr Ser Lys Val Met
185                               190                               195

acc gtg tcc ctg cac aaa ttc tcc cca gga ttt ttc cca gga aca ggt      678
Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe Pro Gly Thr Gly
200                               205                               210

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gac gtg tct gat gtt ggc cta ggg aag gga cgg tac tac agt gta aat Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr Tyr Ser Val Asn 215 220 225	726
gtg ccc att cag gat ggc ata caa gat gaa aaa tat tac cag atc tgt Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr Tyr Gln Ile Cys 230 235 240	774
gaa agt gta cta aag gaa gta tac caa gcc ttt aat ccc aaa gca gtg Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn Pro Lys Ala Val 245 250 255 260	822
gtc tta cag ctg gga gct gac aca ata gct ggg gat ccc atg tgc tcc Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp Pro Met Cys Ser 265 270 275	870
ttt aac atg act cca gtg gga att ggc aag tgt ctt aag tac atc ctt Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu Lys Tyr Ile Leu 280 285 290	918
caa tgg cag ttg gca aca ctc att ttg gga gga gga ggc tat aac ctt Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly Tyr Asn Leu 295 300 305	966
gcc aac acg gct cga tgc tgg aca tac ttg acc ggg gtc atc cta ggg Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly Val Ile Leu Gly 310 315 320	1014
aaa aca cta tcc tct gag atc cca gat cat gag ttt ttc aca gca tat Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe Phe Thr Ala Tyr 325 330 335 340	1062
ggc cct gat tat gtg ctg gaa atc acg cca agc tgc cgg cca gac cgc Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys Arg Pro Asp Arg 345 350 355	1110
aat gag ccc cac cga atc caa caa atc ctc aac tac atc aaa ggg aat Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr Ile Lys Gly Asn 360 365 370	1158
ctg aag cat gtg gtc tag ttgacagaaa gagatcaggt ttccagagct Leu Lys His Val Val 375	1206
gaggagtggg gcctataatg aagacagcgt gtttatgcaa gcagtttgtg gaatttgtga	1266
ctgcaggggaa aatttgaaag aaattacttc ctgaaaattt ccaaggggca tcaagtggca	1326
gctggccttc tgggggtgaag aggcaggcac ccagaggtcc tcaactggac ctagggggaag	1386
aaggagatat cccacattta aagttcttat ttaaaaaaac acacacacac aaatgaaatt	1446
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atgaaacaga tcagaagctg gatgagagca gtcaccagtt tgtagggcag gaggcagctg	1566
agaggcaggg tttgggcctc aggaccatcc aggtggagcc ctgggagaga ggggtactgat	1626
cagcagactg ggaggtgggg agaagtccgc tgggtgttgtt ttagtggttat atatctttgg	1686

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1743

<210> 8

<211> 377

<212> PRT

<213> Homo sapiens

<400> 8

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Val Tyr Ile Tyr Ser Pro Glu Tyr Val Ser Met Cys Asp Ser Leu Ala
20 25 30

Lys Ile Pro Lys Arg Ala Ser Met Val His Ser Leu Ile Glu Ala Tyr
35 40 45

Ala Leu His Lys Gln Met Arg Ile Val Lys Pro Lys Val Ala Ser Met
50 55 60

Glu Glu Met Ala Thr Phe His Thr Asp Ala Tyr Leu Gln His Leu Gln
65 70 75 80

Lys Val Ser Gln Glu Gly Asp Asp Asp His Pro Asp Ser Ile Glu Tyr
85 90 95

Gly Leu Gly Tyr Asp Cys Pro Ala Thr Glu Gly Ile Phe Asp Tyr Ala
100 105 110

Ala Ala Ile Gly Gly Ala Thr Ile Thr Ala Ala Gln Cys Leu Ile Asp
115 120 125

Gly Met Cys Lys Val Ala Ile Asn Trp Ser Gly Gly Trp His His Ala
130 135 140

Lys Lys Asp Glu Ala Ser Gly Phe Cys Tyr Leu Asn Asp Ala Val Leu
145 150 155 160

Gly Ile Leu Arg Leu Arg Arg Lys Phe Glu Arg Ile Leu Tyr Val Asp
165 170 175

Leu Asp Leu His His Gly Asp Gly Val Glu Asp Ala Phe Ser Phe Thr
180 185 190

Ser Lys Val Met Thr Val Ser Leu His Lys Phe Ser Pro Gly Phe Phe
195 200 205

Pro Gly Thr Gly Asp Val Ser Asp Val Gly Leu Gly Lys Gly Arg Tyr
 210 215 220
 Tyr Ser Val Asn Val Pro Ile Gln Asp Gly Ile Gln Asp Glu Lys Tyr
 225 230 235 240
 Tyr Gln Ile Cys Glu Ser Val Leu Lys Glu Val Tyr Gln Ala Phe Asn
 245 250 255
 Pro Lys Ala Val Val Leu Gln Leu Gly Ala Asp Thr Ile Ala Gly Asp
 260 265 270
 Pro Met Cys Ser Phe Asn Met Thr Pro Val Gly Ile Gly Lys Cys Leu
 275 280 285
 Lys Tyr Ile Leu Gln Trp Gln Leu Ala Thr Leu Ile Leu Gly Gly Gly
 290 295 300
 Gly Tyr Asn Leu Ala Asn Thr Ala Arg Cys Trp Thr Tyr Leu Thr Gly
 305 310 315 320
 Val Ile Leu Gly Lys Thr Leu Ser Ser Glu Ile Pro Asp His Glu Phe
 325 330 335
 Phe Thr Ala Tyr Gly Pro Asp Tyr Val Leu Glu Ile Thr Pro Ser Cys
 340 345 350
 Arg Pro Asp Arg Asn Glu Pro His Arg Ile Gln Gln Ile Leu Asn Tyr
 355 360 365
 Ile Lys Gly Asn Leu Lys His Val Val
 370 375

<210> 9
 <211> 1449
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(1449)
 <223> human histone deacetylase-1 (HDAC1) gene

<400> 9
 atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
 1 5 10 15
 ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
 Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro

20	25	30	
cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr 35 40 45			144
cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met 50 55 60			192
acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg 65 70 75 80			240
cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val 85 90 95			288
ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu 100 105 110			336
tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln 115 120 125			384
acg gac atc gct gtg aat tgg gct ggg ggc ctg cac cat gca aag aag Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys 130 135 140			432
tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile 145 150 155 160			480
ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp 165 170 175			528
att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg 180 185 190			576
gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga act Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr 195 200 205			624
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val 210 215 220			672
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile 225 230 235 240			720
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala 245 250 255			768
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly 260 265 270			816

tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc	864
Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val	
275 280 285	
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc	912
Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr	
290 295 300	
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg	960
Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu	
305 310 315 320	
gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac	1008
Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr	
325 330 335	
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac	1056
Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn	
340 345 350	
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag	1104
Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu	
355 360 365	
aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg att	1152
Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile	
370 375 380	
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac	1200
Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp	
385 390 395 400	
cct gac aag cgc atc tcg atc tgc tcc tct gac aaa cga att gcc tgt	1248
Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys	
405 410 415	
gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg ggc cgc aag	1296
Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys	
420 425 430	
aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa	1344
Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu	
435 440 445	
aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa	1392
Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys	
450 455 460	
acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag	1440
Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys	
465 470 475 480	
ttg gcc tga	1449
Leu Ala	

<210> 10
 <211> 482
 <212> PRT

<213> Homo sapiens

<400> 10

Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
1 5 10 15

Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
245 250 255
Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
260 265 270
Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
275 280 285
Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr
290 295 300
Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
305 310 315 320
Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
325 330 335
Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
340 345 350
Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
355 360 365
Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
370 375 380
Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
385 390 395 400
Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
405 410 415
Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys
420 425 430
Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
435 440 445
Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
450 455 460
Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
465 470 475 480

Leu Ala

<210> 11
 <211> 1449
 <212> DNA
 <213> Artificial Sequence
 <220>
 <221> CDS
 <222> (1)..(1449)
 <223> Dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 11
 atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Asp
 1 5 10 15
 ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
 Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
 20 25 30
 cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac 144
 His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
 35 40 45
 cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg 192
 Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 50 55 60
 acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt 240
 Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
 65 70 75 80
 cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt 288
 Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
 85 90 95
 ggt gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg 336
 Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
 100 105 110
 tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag 384
 Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
 115 120 125
 acg gac atc gct gtg aat tgg gct ggg ggc ctg aag ctt gca aag aag 432
 Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys
 130 135 140
 tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc 480
 Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
 145 150 155 160
 ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat 528
 Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
 165 170 175

att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg	576
Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg	
180 185 190	
gtc atg act gtg tcc ttt cat aag tat gga gag tac ttc cca gga act	624
Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr	
195 200 205	
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt	672
Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val	
210 215 220	
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att	720
Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile	
225 230 235 240	
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg	768
Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala	
245 250 255	
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt	816
Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly	
260 265 270	
tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc	864
Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val	
275 280 285	
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc	912
Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Tyr Thr	
290 295 300	
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg	960
Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu	
305 310 315 320	
gat acg gag atc cct aat gag ctt cca tac aat gac tac ttt gaa tac	1008
Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr	
325 330 335	
ttt gga cca gat ttc aag ctc cac atc agt cct tcc aat atg act aac	1056
Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn	
340 345 350	
cag aac acg aat gag tac ctg gag aag atc aaa cag cga ctg ttt gag	1104
Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu	
355 360 365	
aac ctt aga atg ctg ccg cac gca cct ggg gtc caa atg cag gcg att	1152
Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile	
370 375 380	
cct gag gac gcc atc cct gag gag agt ggc gat gag gac gaa gac gac	1200
Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp	
385 390 395 400	
cct gac aag cgc atc tcg atc tgc tcc tct gac aaa cga att gcc tgt	1248
Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys	
405 410 415	
gag gaa gag ttc tcc gat tct gaa gag gag gga gag ggg ggc cgc aag	1296

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys
 420 425 430
 aac tct tcc aac ttc aaa aaa gcc aag aga gtc aaa aca gag gat gaa 1344
 Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
 435 440 445
 aaa gag aaa gac cca gag gag aag aaa gaa gtc acc gaa gag gag aaa 1392
 Lys Glu Lys Asp Pro Glu Lys Lys Lys Glu Val Thr Glu Glu Glu Lys
 450 455 460
 acc aag gag gag aag cca gaa gcc aaa ggg gtc aag gag gag gtc aag 1440
 Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
 465 470 475 480
 ttg gcc tga 1449
 Leu Ala

<210> 12
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dominant negative mutant (H140K, H141L) of human histone deacetylase-1
 (HDAC1) gene

<400> 12
 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
 1 5 10 15

Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
 20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
 35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
 65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
 85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
 100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
 115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys
 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
 145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
 165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
 180 185 190

Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
 195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
 210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
 225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
 245 250 255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
 260 265 270

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
 275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr
 290 295 300

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
 305 310 315 320

Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
 325 330 335

Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
 340 345 350

Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
 355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
 370 375 380

Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
 385 390 395 400

Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
 405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys
 420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
 435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
 450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
 465 470 475 480

Leu Ala

<210> 13
 <211> 1449
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1449)
 <223> Dominant negative mutant (H199L) of human histone deacetylase-1
 (HDAC1)
 gene

<400> 13
 atg gcg cag acg cag ggc acc cgg agg aaa gtc tgt tac tac tac gac 48
 Met Ala Gln Thr Gln Gly Thr Arg Arg Lys Val Cys Tyr Tyr Tyr Asp
 1 5 10 15
 ggg gat gtt gga aat tac tat tat gga caa ggc cac cca atg aag cct 96
 Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
 20 25 30
 cac cga atc cgc atg act cat aat ttg ctg ctc aac tat ggt ctc tac 144
 His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
 35 40 45
 cga aaa atg gaa atc tat cgc cct cac aaa gcc aat gct gag gag atg 192
 Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 50 55 60

acc aag tac cac agc gat gac tac att aaa ttc ttg cgc tcc atc cgt	240
Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg	
65 70 75 80	
cca gat aac atg tcg gag tac agc aag cag atg cag aga ttc aac gtt	288
Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val	
85 90 95	
ggg gag gac tgt cca gta ttc gat ggc ctg ttt gag ttc tgt cag ttg	336
Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu	
100 105 110	
tct act ggt ggt tct gtg gca agt gct gtg aaa ctt aat aag cag cag	384
Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln	
115 120 125	
acg gac atc gct gtg aat tgg gct ggg ggc ctg cac cat gca aag aag	432
Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys	
130 135 140	
tcc gag gca tct ggc ttc tgt tac gtc aat gat atc gtc ttg gcc atc	480
Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile	
145 150 155 160	
ctg gaa ctg cta aag tat cac cag agg gtg ctg tac att gac att gat	528
Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp	
165 170 175	
att cac cat ggt gac ggc gtg gaa gag gcc ttc tac acc acg gac cgg	576
Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg	
180 185 190	
gtc atg act gtg tcc ttt ctt aag tat gga gag tac ttc cca gga act	624
Val Met Thr Val Ser Phe Leu Lys Tyr Gly Glu Tyr Phe Pro Gly Thr	
195 200 205	
ggg gac cta cgg gat atc ggg gct ggc aaa ggc aag tat tat gct gtt	672
Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val	
210 215 220	
aac tac ccg ctc cga gac ggg att gat gac gag tcc tat gag gcc att	720
Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile	
225 230 235 240	
ttc aag ccg gtc atg tcc aaa gta atg gag atg ttc cag cct agt gcg	768
Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala	
245 250 255	
gtg gtc tta cag tgt ggc tca gac tcc cta tct ggg gat cgg tta ggt	816
Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly	
260 265 270	
tgc ttc aat cta act atc aaa gga cac gcc aag tgt gtg gaa ttt gtc	864
Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val	
275 280 285	
aag agc ttt aac ctg cct atg ctg atg ctg gga ggc ggt ggt tac acc	912
Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr	
290 295 300	
att cgt aac gtt gcc cgg tgc agg aca tat gag aca gct gtg gcc ctg	960

Ile	Arg	Asn	Val	Ala	Arg	Cys	Arg	Thr	Tyr	Glu	Thr	Ala	Val	Ala	Leu		
305					310					315					320		
gat	acg	gag	atc	cct	aat	gag	ctt	cca	tac	aat	gac	tac	ttt	gaa	tac		1008
Asp	Thr	Glu	Ile	Pro	Asn	Glu	Leu	Pro	Tyr	Asn	Asp	Tyr	Phe	Glu	Tyr		
				325					330					335			
ttt	gga	cca	gat	ttc	aag	ctc	cac	atc	agt	cct	tcc	aat	atg	act	aac		1056
Phe	Gly	Pro	Asp	Phe	Lys	Leu	His	Ile	Ser	Pro	Ser	Asn	Met	Thr	Asn		
			340					345					350				
cag	aac	acg	aat	gag	tac	ctg	gag	aag	atc	aaa	cag	cga	ctg	ttt	gag		1104
Gln	Asn	Thr	Asn	Glu	Tyr	Leu	Glu	Lys	Ile	Lys	Gln	Arg	Leu	Phe	Glu		
		355					360					365					
aac	ctt	aga	atg	ctg	ccg	cac	gca	cct	ggg	gtc	caa	atg	cag	gcg	att		1152
Asn	Leu	Arg	Met	Leu	Pro	His	Ala	Pro	Gly	Val	Gln	Met	Gln	Ala	Ile		
	370					375					380						
cct	gag	gac	gcc	atc	cct	gag	gag	agt	ggc	gat	gag	gac	gaa	gac	gac		1200
Pro	Glu	Asp	Ala	Ile	Pro	Glu	Glu	Ser	Gly	Asp	Glu	Asp	Glu	Asp	Asp		
385					390				395						400		
cct	gac	aag	cgc	atc	tcg	atc	tgc	tcc	tct	gac	aaa	cga	att	gcc	tgt		1248
Pro	Asp	Lys	Arg	Ile	Ser	Ile	Cys	Ser	Ser	Asp	Lys	Arg	Ile	Ala	Cys		
				405					410					415			
gag	gaa	gag	ttc	tcc	gat	tct	gaa	gag	gag	gga	gag	ggg	ggc	cgc	aag		1296
Glu	Glu	Glu	Phe	Ser	Asp	Ser	Glu	Glu	Glu	Gly	Glu	Gly	Gly	Arg	Lys		
			420					425					430				
aac	tct	tcc	aac	ttc	aaa	aaa	gcc	aag	aga	gtc	aaa	aca	gag	gat	gaa		1344
Asn	Ser	Ser	Asn	Phe	Lys	Lys	Ala	Lys	Arg	Val	Lys	Thr	Glu	Asp	Glu		
		435					440					445					
aaa	gag	aaa	gac	cca	gag	gag	aag	aaa	gaa	gtc	acc	gaa	gag	gag	aaa		1392
Lys	Glu	Lys	Asp	Pro	Glu	Glu	Lys	Lys	Glu	Val	Thr	Glu	Glu	Glu	Lys		
	450					455				460							
acc	aag	gag	gag	aag	cca	gaa	gcc	aaa	ggg	gtc	aag	gag	gag	gtc	aag		1440
Thr	Lys	Glu	Glu	Lys	Pro	Glu	Ala	Lys	Gly	Val	Lys	Glu	Glu	Val	Lys		
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Leu	Ala																

<210> 14
 <211> 482
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 14
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Gly Asp Val Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys Pro
 20 25 30

His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu Tyr
 35 40 45

Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 50 55 60

Thr Lys Tyr His Ser Asp Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
 65 70 75 80

Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
 85 90 95

Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
 100 105 110

Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
 115 120 125

Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
 130 135 140

Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
 145 150 155 160

Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
 165 170 175

Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
 180 185 190

Val Met Thr Val Ser Phe Leu Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
 195 200 205

Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
 210 215 220

Asn Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile
 225 230 235 240

Phe Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala
 245 250 255

Val Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly
 260 265 270

Cys Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val
 275 280 285

Lys Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr
 290 295 300

Ile Arg Asn Val Ala Arg Cys Arg Thr Tyr Glu Thr Ala Val Ala Leu
 305 310 315 320

Asp Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr
 325 330 335

Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn
 340 345 350

Gln Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu
 355 360 365

Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile
 370 375 380

Pro Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp
 385 390 395 400

Pro Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys
 405 410 415

Glu Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys
 420 425 430

Asn Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu
 435 440 445

Lys Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys
 450 455 460

Thr Lys Glu Glu Lys Pro Glu Ala Lys Gly Val Lys Glu Glu Val Lys
 465 470 475 480

Leu Ala

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<210> 15
<211> 1287
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1287)
<223> human histone deacetylase-3 (HDAC3) gene

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Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
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cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc      96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
          20          25          30

cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc      144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
          35          40          45

aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag      192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
          50          55          60

gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc      240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65          70          75          80

ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg      288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
          85          90          95

ttt ccc ggg ctc ttt gag ttc tgc tgc cgt tac aca ggc gca tct ctg      336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
          100          105          110

caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac      384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
          115          120          125

tgg gct ggt ggt ctg cac cat gcc aag aag ttt gag gcc tct ggc ttc      432
Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
          130          135          140

tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac      480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
          145          150          155          160

cac cct cgg gtg ctc tac att gac att gac atc cac cat ggt gac ggc      528
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
          165          170          175

gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtg tcc ttc      576
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
          180          185          190

cac aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa      624
His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu

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195	200	205	
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg 210 215 220			672
gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile 225 230 235 240			720
aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys 245 250 255			768
gga gct gac tct ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser 260 265 270			816
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile 275 280 285			864
cct cta ctc gtg ctg ggt ggt ggt ggt tat act gtc cga aat gtt gcc Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val Ala 290 295 300			912
cgc tgc tgg aca tat gag aca tcg ctg ctg gta gaa gag gcc att agt Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser 305 310 315 320			960
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe 325 330 335			1008
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg 340 345 350			1056
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met 355 360 365			1104
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu 370 375 380			1152
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro 385 390 395 400			1200
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly 405 410 415			1248
gac cat gac aat gac aag gaa agc gat gtg gag att taa Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile 420 425			1287

<210> 16
<211> 428

<212> PRT
<213> Homo sapiens

<400> 16

Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
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His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile

225		230		235		240
Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys	245		250		255	
Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser	260		265		270	
Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile	275		280		285	
Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val Ala	290		295		300	
Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser	305		310		315	
Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe	325		330		335	
Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg	340		345		350	
Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met	355		360		365	
Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu	370		375		380	
Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro	385		390		395	
Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly	405		410		415	
Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile	420		425			

<210> 17
 <211> 1287
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1287)
 <223> Dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 17

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Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe	
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cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc	96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr	
20 25 30	
cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc	144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe	
35 40 45	
aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag	192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu	
50 55 60	
gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc	240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly	
65 70 75 80	
ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg	288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val	
85 90 95	
ttt ccc ggg ctc ttt gag ttc tgc tgc cgt tac aca ggc gca tct ctg	336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu	
100 105 110	
caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac	384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn	
115 120 125	
tgg gct ggt ggt ctg aag ctt gcc aag aag ttt gag gcc tct ggc ttc	432
Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys Phe Glu Ala Ser Gly Phe	
130 135 140	
tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac	480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr	
145 150 155 160	
cac cct cgg gtg ctc tac att gac att gac atc cac cat ggt gac ggg	528
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly	
165 170 175	
gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtg tcc ttc	576
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe	
180 185 190	
cac aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa	624
His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu	
195 200 205	
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg	672
Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg	
210 215 220	
gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc	720
Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile	
225 230 235 240	

aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt	768
Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys	
245 250 255	
gga gct gac tct ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc	816
Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser	
260 265 270	
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc	864
Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile	
275 280 285	
cct cta ctc gtg ctg ggt ggt ggt ggt tat act gtc cga aat gtt gcc	912
Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val Ala	
290 295 300	
cgc tgc tgg aca tat gag aca tcg ctg ctg gta gaa gag gcc att agt	960
Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser	
305 310 315 320	
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc	1008
Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe	
325 330 335	
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc	1056
Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg	
340 345 350	
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg	1104
Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met	
355 360 365	
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc	1152
Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu	
370 375 380	
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct	1200
Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro	
385 390 395 400	
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga	1248
Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly	
405 410 415	
gac cat gac aat gac aag gaa agc gat gtg gag att taa	1287
Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile	
420 425	
<210> 18	
<211> 428	
<212> PRT	
<213> Artificial Sequence	
<220>	
<223> Dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene	
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His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe	35	40	45
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu	50	55	60
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly	65	70	75
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val	85	90	95
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu	100	105	110
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn	115	120	125
Trp Ala Gly Gly Leu Lys Leu Ala Lys Lys Phe Glu Ala Ser Gly Phe	130	135	140
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr	145	150	155
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly	165	170	175
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe	180	185	190
His Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu	195	200	205
Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg	210	215	220
Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile	225	230	235
Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys	245	250	255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser
 260 265 270

Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile
 275 280 285

Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val Ala
 290 295 300

Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser
 305 310 315 320

Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe
 325 330 335

Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg
 340 345 350

Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met
 355 360 365

Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu
 370 375 380

Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro
 385 390 395 400

Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly
 405 410 415

Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile
 420 425

<210> 19
 <211> 1287
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> CDS
 <222> (1)..(1287)
 <223> Dominant negative mutant (H193L) of human histone deacetylase-3
 (HDAC3)
 gene

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 Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe

48

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cac tac gga gct gga cac cct atg aag ccc cat cgc ctg gca ttg acc				96
His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr	20	25	30	
cat agc ctg gtc ctg cat tac ggt ctc tat aag aag atg atc gtc ttc				144
His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe	35	40	45	
aag cca tac cag gcc tcc caa cat gac atg tgc cgc ttc cac tcc gag				192
Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu	50	55	60	
gac tac att gac ttc ctg cag aga gtc agc ccc acc aat atg caa ggc				240
Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly	65	70	75	80
ttc acc aag agt ctt aat gcc ttc aac gta ggc gat gac tgc cca gtg				288
Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val	85	90	95	
ttt ccc ggg ctc ttt gag ttc tgc tgc cgt tac aca ggc gca tct ctg				336
Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu	100	105	110	
caa gga gca acc cag ctg aac aac aag atc tgt gat att gcc att aac				384
Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn	115	120	125	
tgg gct ggt ggt ctg cac cat gcc aag aag ttt gag gcc tct ggc ttc				432
Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe	130	135	140	
tgc tat gtc aac gac att gtg att ggc atc ctg gag ctg ctc aag tac				480
Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr	145	150	155	160
cac cct cgg gtg ctc tac att gac att gac atc cac cat ggt gac ggg				528
His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly	165	170	175	
gtt caa gaa gct ttc tac ctc act gac cgg gtc atg acg gtg tcc ttc				576
Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe	180	185	190	
ctt aaa tac gga aat tac ttc ttc cct ggc aca ggt gac atg tat gaa				624
Leu Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu	195	200	205	
gtc ggg gca gag agt ggc cgc tac tac tgt ctg aac gtg ccc ctg cgg				672
Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg	210	215	220	
gat ggc att gat gac cag agt tac aag cac ctt ttc cag ccg gtt atc				720
Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile	225	230	235	240
aac cag gta gtg gac ttc tac caa ccc acg tgc att gtg ctc cag tgt				768
Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys	245	250	255	

gga gct gac tct ctg ggc tgt gat cga ttg ggc tgc ttt aac ctc agc	816
Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser	
260 265 270	
atc cga ggg cat ggg gaa tgc gtt gaa tat gtc aag agc ttc aat atc	864
Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile	
275 280 285	
cct cta ctc gtg ctg ggt ggt ggt ggt tat act gtc cga aat gtt gcc	912
Pro Leu Leu Val Leu Gly Gly Gly Tyr Thr Val Arg Asn Val Ala	
290 295 300	
cgc tgc tgg aca tat gag aca tcg ctg ctg gta gaa gag gcc att agt	960
Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser	
305 310 315 320	
gag gag ctt ccc tat agt gaa tac ttc gag tac ttt gcc cca gac ttc	1008
Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe	
325 330 335	
aca ctt cat cca gat gtc agc acc cgc atc gag aat cag aac tca cgc	1056
Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg	
340 345 350	
cag tat ctg gac cag atc ctc cag aca atc ttt gaa aac ctg aag atg	1104
Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met	
355 360 365	
ctg aac cat gca cct agt gtc cag att cat gac gtg cct gca gac ctc	1152
Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu	
370 375 380	
ctg acc tat gac agg act gat gag gct gat gca gag gag agg ggt cct	1200
Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro	
385 390 395 400	
gag gag aac tat agc agg cca gag gca ccc aat gag ttc tat gat gga	1248
Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly	
405 410 415	
gac cat gac aat gac aag gaa agc gat gtg gag att taa	1287
Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile	
420 425	

<210> 20
 <211> 428
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3)
 gene

<400> 20
 Met Ala Lys Thr Val Ala Tyr Phe Tyr Asp Pro Asp Val Gly Asn Phe
 1 5 10 15

His Tyr Gly Ala Gly His Pro Met Lys Pro His Arg Leu Ala Leu Thr
20 25 30

His Ser Leu Val Leu His Tyr Gly Leu Tyr Lys Lys Met Ile Val Phe
35 40 45

Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
50 55 60

Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
65 70 75 80

Phe Thr Lys Ser Leu Asn Ala Phe Asn Val Gly Asp Asp Cys Pro Val
85 90 95

Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
100 105 110

Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Ile Asn
115 120 125

Trp Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe
130 135 140

Cys Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Lys Tyr
145 150 155 160

His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
165 170 175

Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe
180 185 190

Leu Lys Tyr Gly Asn Tyr Phe Phe Pro Gly Thr Gly Asp Met Tyr Glu
195 200 205

Val Gly Ala Glu Ser Gly Arg Tyr Tyr Cys Leu Asn Val Pro Leu Arg
210 215 220

Asp Gly Ile Asp Asp Gln Ser Tyr Lys His Leu Phe Gln Pro Val Ile
225 230 235 240

Asn Gln Val Val Asp Phe Tyr Gln Pro Thr Cys Ile Val Leu Gln Cys
245 250 255

Gly Ala Asp Ser Leu Gly Cys Asp Arg Leu Gly Cys Phe Asn Leu Ser

260	265	270
Ile Arg Gly His Gly Glu Cys Val Glu Tyr Val Lys Ser Phe Asn Ile		
275	280	285
Pro Leu Leu Val Leu Gly Gly Gly Gly Tyr Thr Val Arg Asn Val Ala		
290	295	300
Arg Cys Trp Thr Tyr Glu Thr Ser Leu Leu Val Glu Glu Ala Ile Ser		
305	310	315
Glu Glu Leu Pro Tyr Ser Glu Tyr Phe Glu Tyr Phe Ala Pro Asp Phe		
325	330	335
Thr Leu His Pro Asp Val Ser Thr Arg Ile Glu Asn Gln Asn Ser Arg		
340	345	350
Gln Tyr Leu Asp Gln Ile Leu Gln Thr Ile Phe Glu Asn Leu Lys Met		
355	360	365
Leu Asn His Ala Pro Ser Val Gln Ile His Asp Val Pro Ala Asp Leu		
370	375	380
Leu Thr Tyr Asp Arg Thr Asp Glu Ala Asp Ala Glu Glu Arg Gly Pro		
385	390	395
Glu Glu Asn Tyr Ser Arg Pro Glu Ala Pro Asn Glu Phe Tyr Asp Gly		
405	410	415
Asp His Asp Asn Asp Lys Glu Ser Asp Val Glu Ile		
420	425	

<210> 21
 <211> 1458
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1458)
 <223> human N-CoR (RD3) gene

<400>	21	
gaa gtc ctt cag cct gct cca cat caa gtg ata act aat ctc cct gaa		48
Glu Val Leu Gln Pro Ala Pro His Gln Val Ile Thr Asn Leu Pro Glu		
1	5	10
ggc gtt cgg ctt ccg aca act cga cca acc agg cca ccg ccc cct ctc		96
Gly Val Arg Leu Pro Thr Thr Arg Pro Thr Arg Pro Pro Pro Pro Leu		
	20	25
		30

atc ccg tca tcc aaa acc aca gtg gct tca gaa aaa cca tct ttt ata	144
Ile Pro Ser Ser Lys Thr Thr Val Ala Ser Glu Lys Pro Ser Phe Ile	
35 40 45	
atg gga ggc tcc atc tca cag gga aca cca ggc act tat ttg act tct	192
Met Gly Gly Ser Ile Ser Gln Gly Thr Pro Gly Thr Tyr Leu Thr Ser	
50 55 60	
cat aat cag gct tcc tac act caa gaa aca ccc aag ccg tca gta gga	240
His Asn Gln Ala Ser Tyr Thr Gln Glu Thr Pro Lys Pro Ser Val Gly	
65 70 75 80	
tct atc tct ctt gga ctg cca cgg caa cag gaa tct gcc aaa tca gct	288
Ser Ile Ser Leu Gly Leu Pro Arg Gln Gln Glu Ser Ala Lys Ser Ala	
85 90 95	
act ttg ccc tac atc aag cag gaa gaa ttt tct ccc cga agc caa aac	336
Thr Leu Pro Tyr Ile Lys Gln Glu Phe Ser Pro Arg Ser Gln Asn	
100 105 110	
tca caa cct gag ggt ctg ttg gtc agg gcc caa cat gaa ggt gta gtc	384
Ser Gln Pro Glu Gly Leu Leu Val Arg Ala Gln His Glu Gly Val Val	
115 120 125	
aga ggt acc gca gga gcc ata caa gaa gga agt ata act cgg gga act	432
Arg Gly Thr Ala Gly Ala Ile Gln Glu Gly Ser Ile Thr Arg Gly Thr	
130 135 140	
cca acc agc aaa att tca gtg gag agc att cca tcc cta cgg ggc tct	480
Pro Thr Ser Lys Ile Ser Val Glu Ser Ile Pro Ser Leu Arg Gly Ser	
145 150 155 160	
atc act cag ggc acc ccg gct ctg ccc cag act ggc ata cca aca gag	528
Ile Thr Gln Gly Thr Pro Ala Leu Pro Gln Thr Gly Ile Pro Thr Glu	
165 170 175	
gct ttg gtg aag ggg tcc att tcg aga atg ccc att gaa gac agc agt	576
Ala Leu Val Lys Gly Ser Ile Ser Arg Met Pro Ile Glu Asp Ser Ser	
180 185 190	
cct gag aaa ggc aga gag gaa gct gca tcc aaa ggc cat gtt att tat	624
Pro Glu Lys Gly Arg Glu Glu Ala Ala Ser Lys Gly His Val Ile Tyr	
195 200 205	
gaa ggc aaa agt gga cat atc ttg tca tat gat aat att aag aat gcc	672
Glu Gly Lys Ser Gly His Ile Leu Ser Tyr Asp Asn Ile Lys Asn Ala	
210 215 220	
cga gaa ggg act agg agt cca aga aca gct cat gaa atc agt tta aag	720
Arg Glu Gly Thr Arg Ser Pro Arg Thr Ala His Glu Ile Ser Leu Lys	
225 230 235 240	
aga agc tat gaa tca gtg gaa gga aat ata aag caa ggg atg tca atg	768
Arg Ser Tyr Glu Ser Val Glu Gly Asn Ile Lys Gln Gly Met Ser Met	
245 250 255	
agg gag tct cct gta tca gca ccg tta gag ggg ctg ata tgc cga gca	816
Arg Glu Ser Pro Val Ser Ala Pro Leu Glu Gly Leu Ile Cys Arg Ala	
260 265 270	

tta ccc agg ggg agt cct cat tct gac ctc aaa gaa agg act gta ttg	864
Leu Pro Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu	
275 280 285	
tct ggc tcc ata atg cag ggg aca cca aga gca aca act gaa agc ttt	912
Ser Gly Ser Ile Met Gln Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe	
290 295 300	
gaa gat ggc ctt aaa tat ccc aaa caa att aaa agg gaa agt cct ccc	960
Glu Asp Gly Leu Lys Tyr Pro Lys Gln Ile Lys Arg Glu Ser Pro Pro	
305 310 315 320	
ata cga gca ttt gaa ggt gcc att acc aaa gga aaa cca tat gat ggc	1008
Ile Arg Ala Phe Glu Gly Ala Ile Thr Lys Gly Lys Pro Tyr Asp Gly	
325 330 335	
atc acc acc atc aaa gaa atg ggg cgt tcc att cat gag att cca agg	1056
Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro Arg	
340 345 350	
caa gat att tta act cag gaa agt cgg aaa act cca gaa gtg gtc cag	1104
Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr Pro Glu Val Val Gln	
355 360 365	
agc aca cgg ccg ata att gag ggt tcc att tcc cag ggc aca cca ata	1152
Ser Thr Arg Pro Ile Ile Glu Gly Ser Ile Ser Gln Gly Thr Pro Ile	
370 375 380	
aag ttt gac aac aac tca ggt caa tct gcc atc aaa cac aat gtc aaa	1200
Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala Ile Lys His Asn Val Lys	
385 390 395 400	
tcc tta atc acg ggg cct agc aaa cta tcc cgt gga atg cct ccg ctg	1248
Ser Leu Ile Thr Gly Pro Ser Lys Leu Ser Arg Gly Met Pro Pro Leu	
405 410 415	
gaa att gtg cca gag aac ata aaa gtg gta gaa cgg gga aaa tat gag	1296
Glu Ile Val Pro Glu Asn Ile Lys Val Val Glu Arg Gly Lys Tyr Glu	
420 425 430	
gat gtg aaa gca ggc gag acc gtg cgt tcc cgg cac acg tca gtg gta	1344
Asp Val Lys Ala Gly Glu Thr Val Arg Ser Arg His Thr Ser Val Val	
435 440 445	
agc tct ggc ccc tcc gtt ctt agg tcc aca ctg cat gaa gct ccc aaa	1392
Ser Ser Gly Pro Ser Val Leu Arg Ser Thr Leu His Glu Ala Pro Lys	
450 455 460	
gca caa ctg agc cct ggg att tat gat gac acc agt gca cgg agg acc	1440
Ala Gln Leu Ser Pro Gly Ile Tyr Asp Asp Thr Ser Ala Arg Arg Thr	
465 470 475 480	
cct gtg agt tat caa aac	1458
Pro Val Ser Tyr Gln Asn	
485	

<210> 22
 <211> 486
 <212> PRT
 <213> Homo sapiens

<400> 22
 Glu Val Leu Gln Pro Ala Pro His Gln Val Ile Thr Asn Leu Pro Glu
 1 5 10 15

 Gly Val Arg Leu Pro Thr Thr Arg Pro Thr Arg Pro Pro Pro Pro Leu
 20 25 30

 Ile Pro Ser Ser Lys Thr Thr Val Ala Ser Glu Lys Pro Ser Phe Ile
 35 40 45

 Met Gly Gly Ser Ile Ser Gln Gly Thr Pro Gly Thr Tyr Leu Thr Ser
 50 55 60

 His Asn Gln Ala Ser Tyr Thr Gln Glu Thr Pro Lys Pro Ser Val Gly
 65 70 75 80

 Ser Ile Ser Leu Gly Leu Pro Arg Gln Gln Glu Ser Ala Lys Ser Ala
 85 90 95

 Thr Leu Pro Tyr Ile Lys Gln Glu Glu Phe Ser Pro Arg Ser Gln Asn
 100 105 110

 Ser Gln Pro Glu Gly Leu Leu Val Arg Ala Gln His Glu Gly Val Val
 115 120 125

 Arg Gly Thr Ala Gly Ala Ile Gln Glu Gly Ser Ile Thr Arg Gly Thr
 130 135 140

 Pro Thr Ser Lys Ile Ser Val Glu Ser Ile Pro Ser Leu Arg Gly Ser
 145 150 155 160

 Ile Thr Gln Gly Thr Pro Ala Leu Pro Gln Thr Gly Ile Pro Thr Glu
 165 170 175

 Ala Leu Val Lys Gly Ser Ile Ser Arg Met Pro Ile Glu Asp Ser Ser
 180 185 190

 Pro Glu Lys Gly Arg Glu Glu Ala Ala Ser Lys Gly His Val Ile Tyr
 195 200 205

 Glu Gly Lys Ser Gly His Ile Leu Ser Tyr Asp Asn Ile Lys Asn Ala
 210 215 220

 Arg Glu Gly Thr Arg Ser Pro Arg Thr Ala His Glu Ile Ser Leu Lys
 225 230 235 240

Arg Ser Tyr Glu Ser Val Glu Gly Asn Ile Lys Gln Gly Met Ser Met
 245 250 255

Arg Glu Ser Pro Val Ser Ala Pro Leu Glu Gly Leu Ile Cys Arg Ala
 260 265 270

Leu Pro Arg Gly Ser Pro His Ser Asp Leu Lys Glu Arg Thr Val Leu
 275 280 285

Ser Gly Ser Ile Met Gln Gly Thr Pro Arg Ala Thr Thr Glu Ser Phe
 290 295 300

Glu Asp Gly Leu Lys Tyr Pro Lys Gln Ile Lys Arg Glu Ser Pro Pro
 305 310 315 320

Ile Arg Ala Phe Glu Gly Ala Ile Thr Lys Gly Lys Pro Tyr Asp Gly
 325 330 335

Ile Thr Thr Ile Lys Glu Met Gly Arg Ser Ile His Glu Ile Pro Arg
 340 345 350

Gln Asp Ile Leu Thr Gln Glu Ser Arg Lys Thr Pro Glu Val Val Gln
 355 360 365

Ser Thr Arg Pro Ile Ile Glu Gly Ser Ile Ser Gln Gly Thr Pro Ile
 370 375 380

Lys Phe Asp Asn Asn Ser Gly Gln Ser Ala Ile Lys His Asn Val Lys
 385 390 395 400

Ser Leu Ile Thr Gly Pro Ser Lys Leu Ser Arg Gly Met Pro Pro Leu
 405 410 415

Glu Ile Val Pro Glu Asn Ile Lys Val Val Glu Arg Gly Lys Tyr Glu
 420 425 430

Asp Val Lys Ala Gly Glu Thr Val Arg Ser Arg His Thr Ser Val Val
 435 440 445

Ser Ser Gly Pro Ser Val Leu Arg Ser Thr Leu His Glu Ala Pro Lys
 450 455 460

Ala Gln Leu Ser Pro Gly Ile Tyr Asp Asp Thr Ser Ala Arg Arg Thr
 465 470 475 480

Pro Val Ser Tyr Gln Asn
485

<210> 23
<211> 731
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(731)
<223> 5'-flanking region of Human interleukin-2 (IL-2) gene

<400> 23
ctgagtattt aacaatcgca ccctttaaaa aatgtacaat agacattaag agacttaaac 60
agatatataa tcatttttaa ttaaaatagc gttaaacagt acctcaagct caataagcat 120
tttaagtatt ctaatcttag tatttctcta gctgacatgt aagaagcaat ctatcttatt 180
gtatgcaatt agctcattgt gtggataaaa aggtaaaacc attctgaaac aggaaaccaa 240
tacacttctt gtttaaatcaa caaatctaaa cattttattct tttcatctgt ttactcttgc 300
tcttggtccac cacaatatgc tattcacatg ttcagtgtag ttttaggaca aagaaaattt 360
tctgagttac ttttgtatcc ccacccctt aaagaaagga ggaaaaactg tttcatacag 420
aaggcggttaa ttgcatgaat tagagctatc acctaaagtgt gggctaattgt aacaaagagg 480
gatttcacct acatccattc agtcagtctt tgggggttta aagaaattcc aaagagtcac 540
cagaagagga aaaatgaagg taatgttttt tcagacaggt aaagtctttg aaaatatgtg 600
taatatgtaa aacattttga ccccccata atatttttcc agaattaaca gtataaattg 660
catctcttgt tcaagagttc cctatcactc tctttaatca ctactcacag taacctcaac 720
tcttgccaca a 731

<210> 24
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (73)..(506)
<223> 5'-flanking region of Human interleukin-2 (IL-2) gene

<220>
<221> misc_feature
<222> (4)..(9)
<223> a or g or c or t/u, unknown or other

<220>
<221> misc_feature
<222> (12)
<223> a or g or c or t/u, unknown or other

<220>
 <221> . misc_feature
 <222> (56)
 <223> a or g or c or t/u, unknown or other

 <400> 24
 gggnnnnnnng gngatcctct accactatag ggcgaattga atttagcggc cgcganttcg 60
 cccttcgcta gctgctcttg tccaccacaa tatgctattc acatgttcag tgtagtttta 120
 ggacaaagaa aattttctga gttacttttg tatccccacc cccttaaaga aaggaggaaa 180
 aactgtttca tacagaaggc gttaattgca tgaattagag ctatcaccta agtgtgggct 240
 aatgtaacaa agagggattt cacctacatc cattcagtca gtctttgggg gtttaaagaa 300
 attccaaaga gtcatcagaa gaggaaaaat gaaggtaatg ttttttcaga caggtaaagt 360
 ctttgaaaat atgtgtaata tgtaaaacat tttgacaccc ccataatatt tttccagaat 420
 taacagtata aattgcatct cttgttcaag agttccctat cactctcttt aatcactact 480
 cacagtaacc tcaactcctg ccacaagctt cgaagggcga attcggt 527

<210> 25
 <211> 900
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (57)..(875)
 <223> Promoter region of Human GATA-1 gene

 <400> 25
 tgccctcttta ctatagggcg aattgaattt agcggccgcg aattcgccct tgatctatcc 60
 ctggctccca cctcagtttc ccgcctccaa ggcagcatgg cgggcaagaa gttgaggcca 120
 ctgtccctgg gtgttcctac cccacaccc tcaccccaag acagcctgtt actgcggcgc 180
 caacagccac ggtcgcctac atctgataag acttatctgc tgccccaggg caggccggag 240
 ctggcgtaag cccagtgagg gcgctaagt agtgtgcccc tgccctccgc cagcactggc 300
 ctggcctgca ggcttagcct gggcatcaa ggtatccac aggtcttagt tcaaattccag 360
 cagaacctct ctgagcctca ctcttctcac ctgcaaaatg ggtacagcca catcccttct 420
 ctccctgcag ccaggaagac gcacatacac aggagtctag cccacaccgg ccccgacaaa 480
 attaagggtt ttactctctg aaaagcccag tgaagtcatg aaaccatata tgctattttc 540
 atttatcttg gtttcagcct attttgcttg tctggacact acagtccacg ggagcctagg 600
 tcgagcgagg tccaagaatc cccaggggtg gcagggaggg tgggaagaggg cctccagtgc 660
 ccaagaggtg cccacaaagc atgggacccg cccctcccc tggactgccc caccactgg 720
 ggcaccagcc actccctggg gaggagggag gaggggagaag ggagggaggg agggagggag 780

gaagggagcc tcaaaggcca aggccagcca ggacaccccc tgggatcaca ctgagcttgc 840
cacatcccca aggcggccga accctccgca accaccaaag cttataaggc cgaattcggt 900

<210> 26
<211> 660
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (11)..(647)
<223> Promoter region of Human GATA-1 gene

<400> 26
ttatggtacc accccagaag atgccaggag ggagtgagcc agtcagggaa ggcttccgag 60
aagagaggac attgaagaag agtctcaaac ttaggcctga cggagaagac gcgcggccag 120
gacacccac ccccgccctc gtctcccca aagcctgac tggccccact gattccctta 180
tctgcccact ccagctgcc tccttgctgg ctgaactgtc gccgcagact tctgagcctg 240
cgccccctcc acgggggatgg gggagggaaat ggggtgaggc ctggcctcac agcctcgggg 300
tttccagctc ttgctggagg cagggtctctg gggcgcccta ctctcacc ttggcttctc 360
ttctgagcg ctctgtgtc tccagaaatg aagaaatggg gtgagtccag cggccaaacc 420
cttgtcttag ctcttagaca tgctcgagc ctgccattcc ctgtgaggac agatttcctt 480
atgttgcgac cgctgcttct aataataata atgatgatga taattcccat ttacagagca 540
caccatttat ggtgtgccag caggccctgt gctgagtggg tcctaccac gtgggggggt 600
aggactttac ccgttttcca gatgaagaaa ctgaggctca gagggcgcta gcataagggc 660

<210> 27
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2
(IL-2) gene

<400> 27
tcgctagcct gagtatttaa caatcgcacc ct 32

<210> 28
<211> 30
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2
(IL-2) gene

<400> 28
cgaagcttgt ggcaggagtt gaggttactg 30

<210> 29
<211> 777
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(777)
<223> Corresponding to the sequence (+661 to +1437) in the GenBank database
(Accession: HSIL05)

<400> 29
atcagtatcc ttgaatcgaa acctttttct gagtatttaa caatcgcacc ctttaaaaaa 60
tgtacataga cattaagaga cttaaacaga tatataatca ttttaaatta aaatagcggt 120
aaacagtacc tcaagctcaa taagcatttt aagtattcta atcttagtat ttctctagct 180
gacatgtaag aagcaatcta tcttattgta tgcaattagc tctttgtgtg gataaaaagg 240
taaaaccatt ctgaaacagg aaaccaatac acttcctggt taatcaacaa atctaaacat 300
ttattctttt catctgttta ctcttgctct tgtccaccac aatatgctat tcacatgttc 360
agtgtagttt tatgacaaag aaaattttct gagttacttt tgtatcccca cccccttaa 420
gaaaggagga aaaactgttt catacagaag gcgttaattg catgaattag agctatcacc 480
taagtgtggg ctaatgtaac aaagagggat ttcacctaca tccattcagt cagtctttgg 540
gggttttaaag aaattccaaa gagtcatcag aagaggaaaa atgaaggtaa tgttttttca 600
gactggtaaa gtctttgaaa atatgtgtaa tatgtaaaac attttgacac ccccataata 660
tttttccaga attaacagta taaattgcat ctcttggttca agagttccct atcactcttt 720
aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctctgt 777

<210> 30
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer for amplifying the 5'-flanking region of Human interleukin-2
(IL-2) gene

<400> 30
cgctagctgc tcttgtccac cacaatatgc 30

<210> 31
 <211> 538
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)..(538)
 <223> Corresponding to the sequence (+901 to +1438) in the GenBank database
 (Acession: HSIL05)

<400> 31
 taaaaccatt ctgaaacagg aaaccaatac acttcctggt taatcaacaa atctaaacat 60

 ttattctttt catctgttta ctcttgctct tgtccaccac aatatgctat tcacatgttc 120

 agtgtagttt tatgacaaag aaaattttct gagttacttt tgtatcccca cccctttaa 180

 gaaaggagga aaaactgttt catacagaag gcgttaattg catgaattag agctatcacc 240

 taagtgtggg ctaatgtaac aaagagggat ttcacctaca tccattcagt cagtctttgg 300

 gggttttaaag aaattccaaa gagtcatcag aagaggaaaa atgaaggtaa tgttttttca 360

 gactggtaaa gtctttgaaa atatgtgtaa tatgtaaaac attttgacac ccccataata 420

 tttttccaga attaacagta taaattgcat ctcttggtca agagttccct atcactcttt 480

 aatcactact cacagtaacc tcaactcctg ccacaatgta caggatgcaa ctctgtgc 538

<210> 32
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 32
 atagatctat ccctggctcc cacctcag 28

<210> 33
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying the promoter region of Human GATA-1 gene

<400> 33
 ataagctttg gtggttgagg agggttcg 28

<210> 34
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>

<223> PCR primer for amplifying the promoter region of Human GATA-1 gene
 <400> 34
 atggtaccac cccagaagat gccaggag 28

 <210> 35
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer for amplifying the promoter region of Human GATA-1 gene
 <400> 35
 atgctagcgc cctctgagcc tcagtttc 28

 <210> 36
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer for amplifying a human histone deacetylase-1 (HDAC1) gene
 <400> 36
 gaggaattca agatggcgca gac 23

 <210> 37
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer for amplifying a human histone deacetylase-1 (HDAC1) gene
 <400> 37
 ggagcggccg cttcaggcca acttg 25

 <210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene
 <400> 38
 ggggatccat ggcgtaacgt caag 24

 <210> 39
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> PCR primer for amplifying a human histone deacetylase-2 (HDAC2) gene

<400> 39
 ggtgcggccg ccaaattcag gggttgctg 29

<210> 40
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 40
 ccggatccac catggccaag ac 22

<210> 41
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 41
 gcagcgccg ccactcttaa atctccac 28

<210> 42
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-4 (HDAC4) gene

<400> 42
 gggaattcat gagctcccaa agccatcc 28

<210> 43
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-4 (HDAC4) gene

<400> 43
 aaggcgccgc agcttcgagg gagtgctac 29

<210> 44
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-5 (HDAC5) gene

<400> 44
 ggcaagctta tgaactctcc caacgag 27

<210> 45
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-5 (HDAC5) gene

<400> 45
 gggcggccgc gtcacagggc aggctcctg 29

<210> 46
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-6 (HDAC6) gene

<400> 46
 gcgaagctta tgacctcaac cggccag 27

<210> 47
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-6 (HDAC6) gene

<400> 47
 gcatgcggcc gcttagtgtg ggtggggcat atc 33

<210> 48
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-7 (HDAC7) gene

<400> 48
 cgaattcagc cgcagcccat ggacct 26

<210> 49
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-7 (HDAC7) gene

<400> 49
 cggtaccctg tgcacccgga tcacgg 26

<210> 50
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-8 (HDAC8) gene

<400> 50
 cgaattcttt aagcggaaga tggagg 26

<210> 51
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-8 (HDAC8) gene

<400> 51
 aggtaccgac cacatgcttc agattc 26

<210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying a human histone deacetylase-3 (HDAC3) gene

<400> 52
 ctgaattcac catggccaag accg 24

<210> 53
 <211> 61
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for adding a Flag sequence to a human histone deacetylase-3 (HDAC3) gene

<400> 53
 gggcgggcgc ctacttgtca tcgtcgtcct tgtaatcggg accaatctcc acatcgcttt 60

c 61

<210> 54
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Flag sequence

<400> 54

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 55

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for adding a Kpn I site to a human histone deacetylase-1 (HDAC1) gene

<400> 55

atcggtaccg gccaaacttga cctcctcctt g. 31

<210> 56

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for adding a Kpn I site to a human histone deacetylase-2 (HDAC2) gene

<400> 56

atcggtaccg ggggttgctga gctgttctg 29

<210> 57

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for adding a Bgl II site to a human histone deacetylase-4 (HDAC4) gene

<400> 57

gatagatctc aggggcggct cctcttc 27

<210> 58

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence having a Flag nucleotide sequence

<400> 58

aattcctgca gagatctgat tacaaggacg acgatgacaa gtaggc 46

<210> 59

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide sequence having a Flag nucleotide sequence

<400> 59
ggccgcctac ttgtcatcgt cgtccttgta atcagatctc tgcagg 46

<210> 60
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 60
cagtgacacc atatggaacg agg 23

<210> 61
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 61
gcaagctttc caggggggcg 20

<210> 62
<211> 20
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 62
ccccctggaa agcttgcgga 20

<210> 63
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H802K, H803L) of human histone deacetylase-4 (HDAC4) gene

<400> 63
 gacatgtaca ggacgctagg gt 22

<210> 64
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H863L) of human histone deacetylase-4 (HDAC4) gene

<400> 64
 cctgtacatg tccctccttc g 21

<210> 65
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H863L) of human histone deacetylase-4 (HDAC4) gene

<400> 65
 atagatctag acaggggcgg 20

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 66
 gaggaattca agatggcgca gac 23

<210> 67
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 67
 ctcggaacttc tttgcaagct tcagg 25

<210> 68
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 68
gggcctgaag cttgcaaaga agtc 24

<210> 69
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H140K, H141L) of human histone deacetylase-1 (HDAC1) gene

<400> 69
gtgaatatca atgtcaatgt acagc 25

<210> 70
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 70
gacggcgtgg aagaggcctt c 21

<210> 71
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 71
gaagtactct ccatacttaa gaaagg 26

<210> 72
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 72

ctgtgtcctt tcttaagtat ggagag 26

<210> 73
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H199L) of human histone deacetylase-1 (HDAC1) gene

<400> 73
 tctcggagcg ggtagttaac ag 22

<210> 74
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 74
 aacccagctg aacaacaaga tctg 24

<210> 75
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 75
 ctcaaacttc ttggcaagct tcagac 26

<210> 76
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 76
 tgggtggtctg aagcttgcca agaag 25

<210> 77
 <211> 21
 <212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H134K, H135L) of human histone deacetylase-3 (HDAC3) gene

<400> 77
cccgtcacca tggatgatgt c 21

<210> 78
<211> 23
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 78
tgacattgac atccaccatg gtg 23

<210> 79
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 79
gaagtaattt ccgtacttaa ggaagg 26

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 80
tgtccttcct taagtacgga aattac 26

<210> 81
<211> 22
<212> DNA
<213> Artificial Sequence

<220>

<223> PCR primer for creating a dominant negative mutant (H193L) of human histone deacetylase-3 (HDAC3) gene

<400> 81
gagcacaatg cacgtgggtt gg 22

<210> 82
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying RD3 sequence of human N-CoR gene

<400> 82
 gggatccgtg aagtccttca gcctgctcc 29

<210> 83
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer for amplifying RD3 sequence of human N-CoR gene

<400> 83
 tgcggccgcc atgggtgagc ctctggaca 29

<210> 84
 <211> 960
 <212> DNA
 <213> homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(960)
 <223> Corresponding to the sequence (+5281 to +6240) in the GenBank database
 (Accession: AF196971)

<400> 84
 gcctctgtct ctcccaactcc acccctttcc ttctctaccc tatcccaactc ctcgaggaat 60
 catccctggc tcccaccta gtttcccgcc tccaaggcag catggcgggc aagaagttga 120
 ggccactgtc cctgggtggt cctaccccca caccctcacc ccaagacagc ctgttactgc 180
 ggcgccaaca gccacggtcg cctacatctg ataagactta tctgctgccc cagggcaggc 240
 cggagctggc gtaagcccca gtggggcgct aagtgagtgt gccctgcct cccgccagca 300
 ctggcctggc ctgcaggctt agcctgggtc atcaaggtat cccacaggct ctagttcaaa 360
 tccagcagaa cctctctgag cctcactctt ctcacctgca aaatgggtac agccacatcc 420
 cttctctccc tgcagccagg aagacgcaca tacacaggag tctagccac accggccccg 480
 cacaaattaa gggctttact ctctgaaaag ccagtgaaag tcatgaaacc atatctgcta 540
 ttttcattta tcttggtttc agcctatctt gcttgctctg acactacagt ccacggggagc 600
 ctaggtcgag cgagggtcaa gaatccccag ggtgggcagg gaggggtggaa gagggcctcc 660
 agtgcccaag aggtgcccc caagcatggg acccgcccc tccctggac tgccccaccc 720

actggggcac cagccactcc ctggggagga gggaggaggg agaaggagg gagggagga 780
 gggaggaagg gagcctcaaa ggccaaggcc agccaggaca ccccttgga tcacactgag 840
 cttgccacat cccaaggcg gccgaaccct ccgcaaccac cagcccaggt cagtctcagc 900
 cccagagag ccccccacaa ggcaaccctg ggctgctgc ccctaccctt atgcttctc 960

<210> 85

<211> 720

<212> DNA

<213> homo sapiens

<220>

<221> misc_feature

<222> (1)..(720)

<223> Corresponding to the sequence (+2321 to +3040) in the GenBank database
 (Accession: AF196971)

<400> 85

gtacaaatgc catggggcct ggaccaagca ggggctctag aaccccagaa gatgccagga 60
 gggagtgagc cagtcaggga aggcttccga gaagagagga cattgaagaa gagtctcaaa 120
 cttaggcctg acggagaaga cgcgcggcca ggacacccca ccccgccct cgtctcccc 180
 aaagcctgat ctggccccac tgattccctt atctgccac tcccagctgc ctccctgctg 240
 gctgaactgt cgccgcagac ttctgagcct gcgccccctc cacggggatg ggggagggaa 300
 tggggtgagg cctggcctca cagcctcggg gtttccagct cttgctggag gcagggctct 360
 ggggcgccct actcctcacc cttggcttct cttcctgagc gctctgtgct ctccagaaat 420
 gaagaaatgg ggtgagtcca gcggccaaac cttgtctta gctcttagac atgcctcgag 480
 cctgccattc cctgtgagga cagatttccc tatgttgca ccgctgcttc taataataat 540
 aatgatgatg ataattccca ttacagagc acaccattta tgggtgtgcca gcaggccctg 600
 tgctgagtgg ttctaccca cgtggggggc taggacttta cccgttttcc agatgaagaa 660
 actgaggctc agagggcgtc tggcccagga atcacacagc aaatcacaca gcaaatcaga 720

<210> 86

<211> 12

<212> DNA

<213> homo sapiens

<220>

<221> misc_feature

<222> (1)..(12)

<223> Palindrome sequence found on the 3' side of the GATA-E-box motif in
 promoter region of human GATA-1 gene

<400> 86

ctgtggccac ag

12